<u>RAW SEQUENCE LISTING</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/030,464A_
Source: _1FW16_
Date Processed by STIC: _9/26/05_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 09/26/2005
PATENT APPLICATION: US/10/030,464A   TIME: 09:41:33

Input Set : A:\215110.ST25.txt.txt
Output Set: N:\CRF4\09262005\J030464A.raw

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 3 <110> APPLICANT: Feussner, Ivo
 4        Hornung, Ellen
 5        Rosahl, Sabine
 7 <120> TITLE OF INVENTION: 11-ARACHIDONATE-LIPOXYGENASE MUTANTS
 9 <130> FILE REFERENCE: 215110
11 <140> CURRENT APPLICATION NUMBER: US 10/030,464A
12 <141> CURRENT FILING DATE: 2002-05-22
14 <150> PRIOR APPLICATION NUMBER: PCT/EP00/06539
15 <151> PRIOR FILING DATE: 2000-07-10
17 <150> PRIOR APPLICATION NUMBER: DE 199 31 819.0
18 <151> PRIOR FILING DATE: 1999-07-08
20 <160> NUMBER OF SEQ ID NOS: 3
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 61
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Primer
32 <400> SEQUENCE: 1
33 gctggtgggg ttcttgagag tacattcttt ccttcgaaat ttgccatgga aatgtcagct    60
35 g                                                                    61
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 61
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Primer
46 <400> SEQUENCE: 2
47 cagcgtacat ttccatggca aatttcgaag gaaagaatgt actctcaaga accccaccag    60
49 c                                                                    61
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 857
54 <212> TYPE: PRT
55 <213> ORGANISM: Solanum tuberosum
57 <400> SEQUENCE: 3
59 Gln Ile Val Gly Gly Leu Ile Gly Gly His His Asp Ser Lys Lys Val
60 1               5                   10                  15
63 Lys Gly Thr Val Val Met Met Lys Lys Asn Ala Leu Asp Phe Thr Asp
64              20                  25                  30
67 Leu Ala Gly Ser Leu Thr Asp Lys Ile Phe Glu Ala Leu Gly Gln Lys
68          35                  40                  45
71 Val Ser Phe Gln Leu Ile Ser Ser Val Gln Ser Asp Pro Ala Asn Gly
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72      50                      55                      60
75 Leu Gln Gly Lys His Ser Asn Pro Ala Tyr Leu Glu Asn Phe Leu Phe
76 65                      70                      75                      80
79 Thr Leu Thr Pro Leu Ala Ala Gly Glu Thr Ala Phe Gly Val Thr Phe
80                      85                      90                      95
83 Asp Trp Asn Glu Glu Phe Gly Val Pro Gly Ala Phe Ile Ile Lys Asn
84                      100                     105                     110
87 Thr His Ile Asn Glu Phe Phe Leu Lys Ser Leu Thr Leu Glu Asp Val
88                      115                     120                     125
91 Pro Asn His Gly Lys Val His Phe Val Cys Asn Ser Trp Val Tyr Pro
92      130                     135                     140
95 Ser Phe Arg Tyr Lys Ser Asp Arg Ile Phe Phe Ala Asn Gln Pro Tyr
96 145                     150                     155                     160
99 Leu Pro Ser Glu Thr Pro Glu Leu Leu Arg Lys Tyr Arg Glu Asn Glu
100                     165                     170                     175
103 Leu Leu Thr Leu Arg Gly Asp Gly Thr Gly Lys Arg Glu Ala Trp Asp
104                     180                     185                     190
107 Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Leu Gly Asn Pro Asp Gln
108                     195                     200                     205
111 Gly Glu Gln Asn Val Arg Thr Thr Leu Gly Gly Ser Ala Asp Tyr Pro
112      210                     215                     220
115 Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro Pro Thr Arg Thr Asp Pro
116 225                     230                     235                     240
119 Lys Ser Glu Ser Arg Ile Pro Leu Ile Leu Ser Leu Asp Ile Tyr Val
120                     245                     250                     255
123 Pro Arg Asp Glu Arg Phe Gly His Leu Lys Met Ser Asp Phe Leu Thr
124      260                     265                     270
127 Tyr Ala Leu Lys Ser Ile Val Gln Phe Ile Leu Pro Glu Leu His Ala
128      275                     280                     285
131 Leu Phe Asp Gly Thr Pro Asn Glu Phe Asp Ser Phe Glu Asp Val Leu
132      290                     295                     300
135 Arg Leu Tyr Glu Gly Gly Ile Lys Leu Pro Gln Gly Pro Leu Phe Lys
136 305                     310                     315                     320
139 Ala Leu Thr Ala Ala Ile Pro Leu Glu Met Met Lys Glu Leu Leu Arg
140                     325                     330                     335
143 Thr Asp Gly Glu Gly Ile Leu Arg Phe Pro Thr Pro Leu Val Ile Lys
144      340                     345                     350
147 Asp Ser Lys Thr Ala Trp Arg Thr Asp Glu Glu Phe Ala Arg Glu Met
148      355                     360                     365
151 Leu Ala Gly Val Asn Pro Ile Ile Ile Ser Arg Leu Gln Glu Phe Pro
152      370                     375                     380
155 Pro Lys Ser Lys Leu Asp Pro Glu Ala Tyr Gly Asn Gln Asn Ser Thr
156 385                     390                     395                     400
159 Ile Thr Ala Glu His Ile Glu Asp Lys Leu Asp Gly Leu Thr Val Asp
160                     405                     410                     415
163 Glu Ala Met Asn Asn Asn Lys Leu Phe Ile Leu Asn His His Asp Val
164      420                     425                     430
167 Leu Ile Pro Tyr Leu Arg Arg Ile Asn Thr Thr Thr Thr Lys Thr Tyr
168      435                     440                     445
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171 Ala Ser Arg Thr Leu Leu Phe Leu Gln Asp Asn Gly Ser Leu Lys Pro
172     450                 455                 460
175 Leu Ala Ile Glu Leu Ser Leu Pro His Pro Asp Gly Asp Gln Phe Gly
176 465                 470                 475                 480
179 Val Ile Ser Lys Val Tyr Thr Pro Ser Asp Gln Gly Val Glu Ser Ser
180                 485                 490                 495
183 Ile Trp Gln Leu Ala Lys Ala Tyr Val Ala Val Asn Asp Ser Gly Val
184                 500                 505                 510
187 His Gln Leu Ile Ser His Trp Leu Asn Thr His Ala Val Ile Glu Pro
188         515                 520                 525
191 Phe Val Ile Ala Thr Asn Arg Gln Leu Ser Val Leu His Pro Ile His
192     530                 535                 540
195 Lys Leu Leu Tyr Pro His Phe Arg Asp Thr Met Asn Ile Asn Ala Met
196 545                 550                 555                 560
199 Ala Arg Gln Ile Leu Ile Asn Ala Gly Gly Val Leu Glu Ser Thr Val
200             565                 570                 575
203 Phe Pro Ser Lys Phe Ala Met Glu Met Ser Ala Val Val Tyr Lys Asp
204             580                 585                 590
207 Trp Val Phe Pro Asp Gln Ala Leu Pro Ala Asp Leu Val Lys Arg Gly
208     595                 600                 605
211 Val Ala Val Glu Asp Ser Ser Ser Pro His Gly Val Arg Leu Leu Ile
212     610                 615                 620
215 Glu Asp Tyr Pro Tyr Ala Val Asp Gly Leu Glu Ile Trp Ser Ala Ile
216 625                 630                 635                 640
219 Lys Ser Trp Val Thr Asp Tyr Cys Ser Phe Tyr Tyr Gly Ser Asp Glu
220             645                 650                 655
223 Glu Ile Leu Lys Asp Asn Glu Leu Gln Ala Trp Trp Lys Glu Leu Arg
224             660                 665                 670
227 Glu Val Gly His Gly Asp Lys Lys Asn Glu Pro Trp Trp Pro Glu Met
228         675                 680                 685
231 Glu Thr Pro Gln Glu Leu Ile Asp Ser Cys Thr Thr Ile Ile Trp Ile
232     690                 695                 700
235 Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly Gln Tyr Pro Tyr Ala
236 705                 710                 715                 720
239 Gly Tyr Leu Pro Asn Arg Pro Thr Val Ser Arg Arg Phe Met Pro Glu
240             725                 730                 735
243 Pro Gly Thr Pro Glu Tyr Glu Glu Leu Lys Lys Asn Pro Asp Lys Ala
244             740                 745                 750
247 Phe Leu Lys Thr Ile Thr Ala Gln Leu Gln Thr Leu Leu Gly Val Ser
248         755                 760                 765
251 Leu Ile Glu Ile Leu Ser Arg His Thr Thr Asp Glu Ile Tyr Leu Gly
252     770                 775                 780
255 Gln Arg Glu Ser Pro Glu Trp Thr Lys Asp Lys Glu Pro Leu Ala Ala
256 785                 790                 795                 800
259 Phe Asp Lys Phe Gly Lys Lys Leu Thr Asp Ile Glu Lys Gln Ile Ile
260             805                 810                 815
263 Gln Arg Asn Gly Asp Asn Ile Leu Thr Asn Arg Ser Gly Pro Val Asn
264             820                 825                 830
267 Ala Pro Tyr Thr Leu Leu Phe Pro Thr Ser Glu Gly Gly Leu Thr Gly
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268            835                840                845
271 Lys Gly Ile Pro Asn Ser Val Ser Ile
272     850                855
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2

VERIFICATION SUMMARY   DATE: 09/26/2005
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